Data Standards for Microarray Data

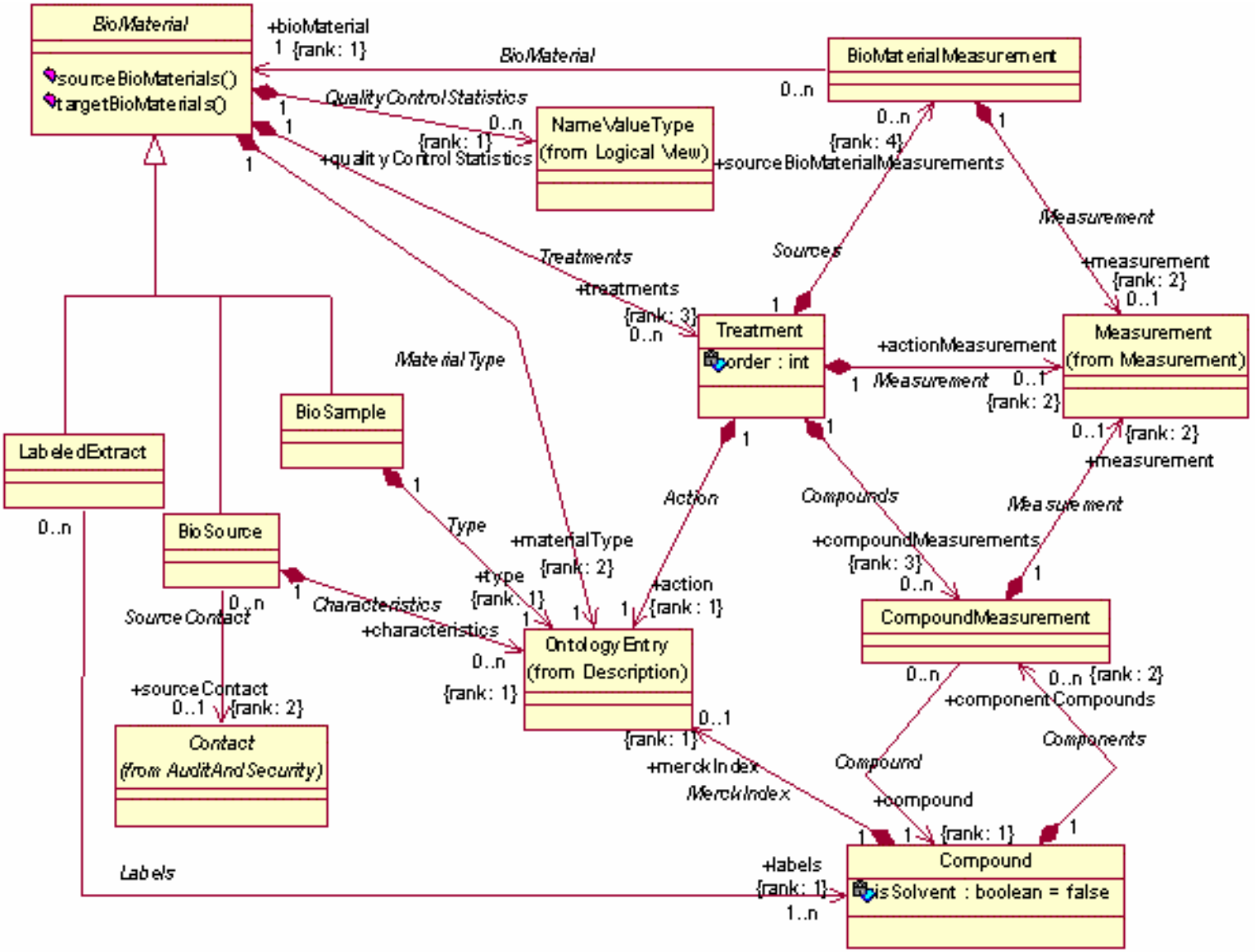
Components of MAGE-OM

- Array design and manufacture
- Biological sample source detail and generation
- Actual data and images from array hybridizations
- Clustering results
- Experimental design details

MAGE Design Team

- MGED Members (mostly Stewart, Spellman, and Sarkans)
- Rosetta (Michael Miller and Doug Bassett)
- Agilent (Charles Troup)
- Affymetrix (Steve Chervitz and Derek Bernhart)
- NetGenics/Lion Bioscience (Scott Markel)

BioMaterial



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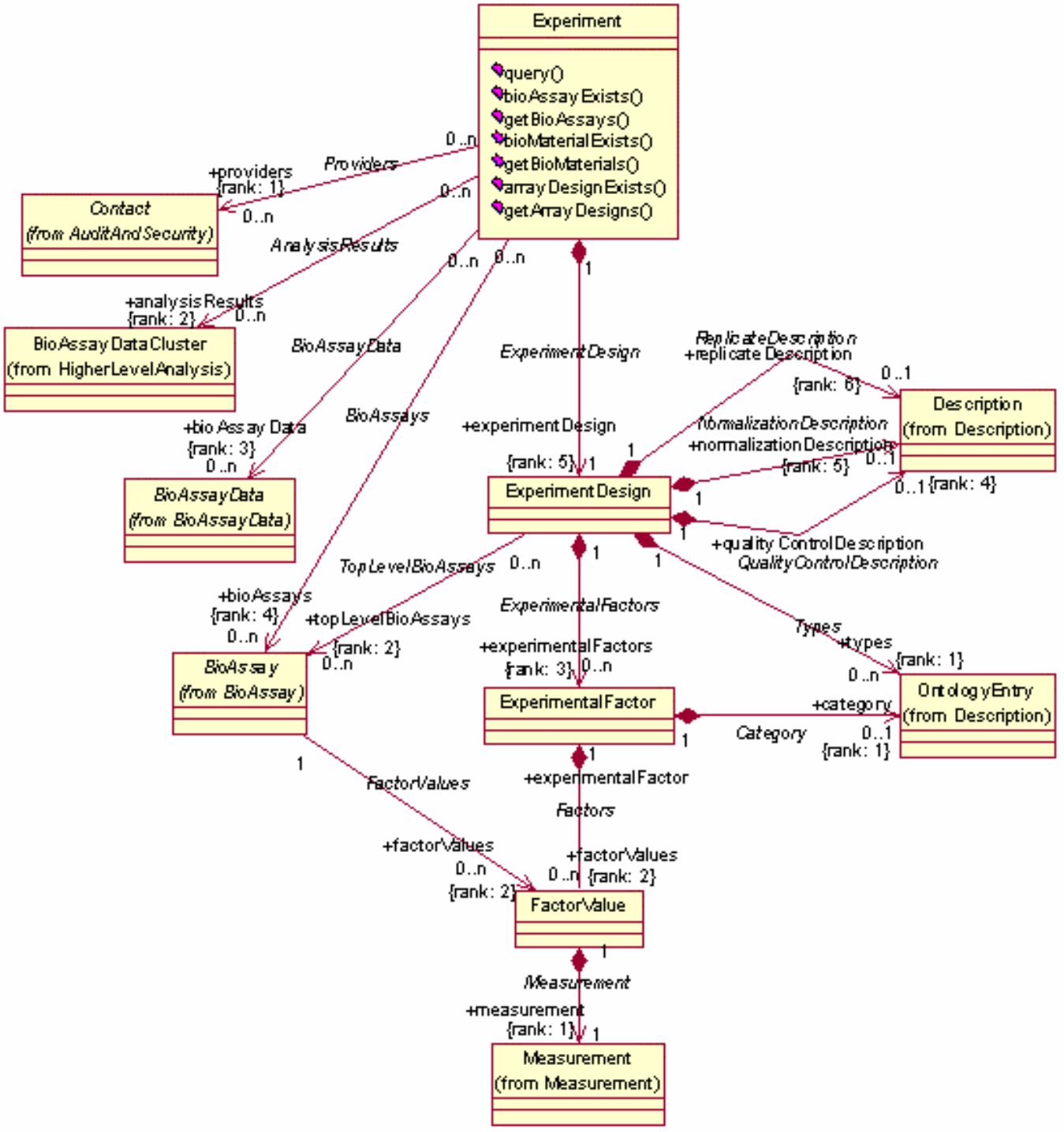

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The MAGEstk

- Freely available software collection (MIT open source license)
- Includes
  - MAGE-ML Parsers for:
    - Perl -- Complete and functional
    - Java -- Complete and functional
  - Data annotation tool (MIAME Express)

MGED Ontology (MO)

- Purpose
  - Provide standard terms for the annotation of microarray experiments
- Benefits
  - Unambiguous description of how the experiment was performed
  - Structured queries can be generated
- Ontology concepts derived from the MIAME guidelines/MAGE-OM

Relationship of MO to MAGE-OM

- MO class hierarchy follows that of MAGE-OM
  - Association to OntologyEntry
- MO provides terms for these associations by:
  - Instances internal to MO
  - Instances from external ontologies
    - Take advantage of existing ontologies

MAGE and MO

Usage of

SurfaceType

Classes

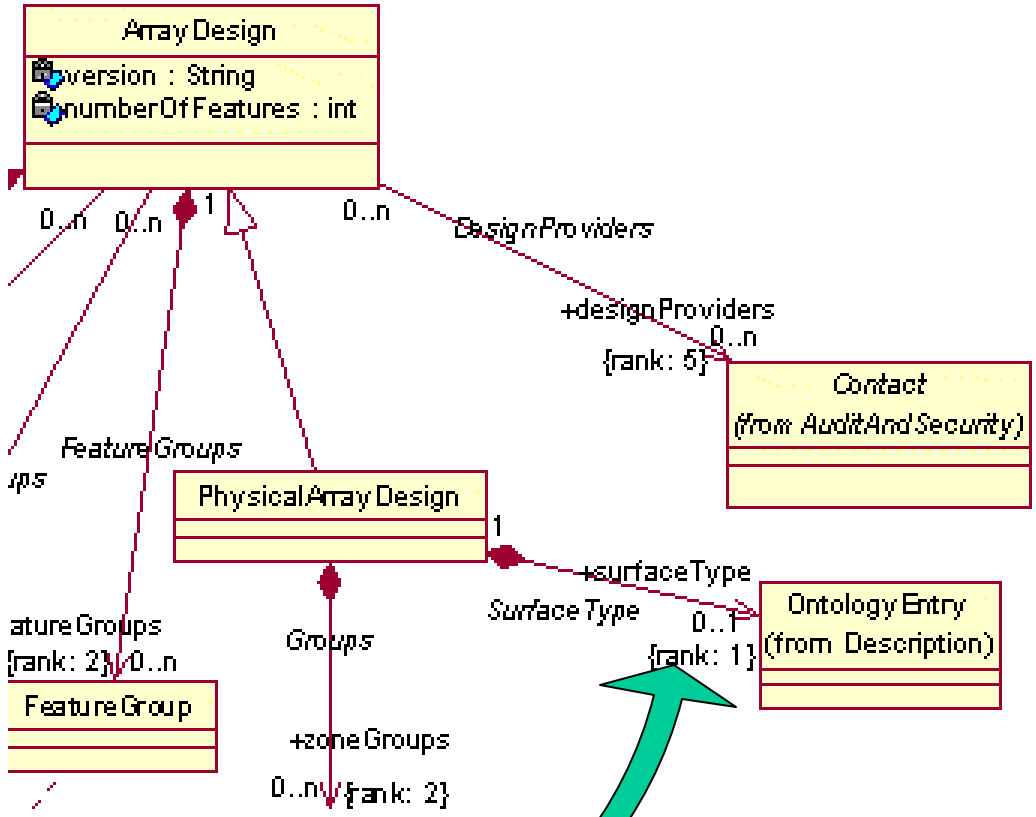
C PhysicalArrayDesign

Individuals

I polylysine

I aminosilane

I unknown_surface_type



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